Rameen Beroukhim

List of Publications by Year in Descending Order

145 papers	51,790 citations	88 h-index	153 g-index
153 ext. papers	67,132 ext. citations	24.5 avg, IF	6.14 L-index

#	Paper	IF	Citations
145	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation.. *Nature Communications*, **2022**, 13, 604	17.4	0
144	Quantification of aneuploidy in targeted sequencing data using ASCETS. *Bioinformatics*, **2021**, 37, 2461-2463	7.9	4
143	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
142	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. *STAR Protocols*, **2021**, 2, 100483	1.4	0
141	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. *Nature*, **2021**, 590, 486-491	50.4	34
140	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. *Nature Communications*, **2020**, 11, 2517	17.4	21
139	Tumor Interferon Signaling Is Regulated by a lncRNA INCR1 Transcribed from the PD-L1 Locus. *Molecular Cell*, **2020**, 78, 1207-1223.e8	17.6	18
138	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
137	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
136	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
135	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. *Cell*, **2020**, 183, 197-210.e32	56.2	45
134	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
133	Mechanisms and therapeutic implications of hypermutation in gliomas. *Nature*, **2020**, 580, 517-523	50.4	172
132	Buparlisib in Patients With Recurrent Glioblastoma Harboring Phosphatidylinositol 3-Kinase Pathway Activation: An Open-Label, Multicenter, Multi-Arm, Phase II Trial. *Journal of Clinical Oncology*, **2019**, 37, 741-750	2.2	64
131	Molecular profiling and targeted therapy in pediatric gliomas: review and consensus recommendations. *Neuro-Oncology*, **2019**, 21, 968-980	1	26
130	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. *Nature Communications*, **2019**, 10, 3731	17.4	17
129	MCL1 and DEDD Promote Urothelial Carcinoma Progression. *Molecular Cancer Research*, **2019**, 17, 1294-1304	6.3	2

128	Longitudinal molecular trajectories of diffuse glioma in adults. *Nature*, **2019**, 576, 112-120	50.4	151
127	Genomic evolution of cancer models: perils and opportunities. *Nature Reviews Cancer*, **2019**, 19, 97-109	31.3	104
126	Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. *Clinical Cancer Research*, **2019**, 25, 334-345	12.9	9
125	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
124	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
123	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
122	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
121	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
120	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
119	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
118	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
117	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
116	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
115	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
114	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
113	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
112	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. *Neuro-Oncology*, **2018**, 20, 873-884	1	63
111	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150

110	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. *Nature Medicine*, **2018**, 24, 679-690	50.5	659
109	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
108	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
107	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. *Cancer Cell*, **2018**, 33, 706-720.e9	24.3	275
106	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
105	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
104	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
103	SvABA: genome-wide detection of structural variants and indels by local assembly. *Genome Research*, **2018**, 28, 581-591	9.7	149
102	Genetic and transcriptional evolution alters cancer cell line drug response. *Nature*, **2018**, 560, 325-330	50.4	379
101	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
100	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. *Cell*, **2018**, 174, 433-447.e19	56.2	155
99	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
98	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
97	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, **2017**, 31, 181-193	24.3	350
96	Clinical Identification of Oncogenic Drivers and Copy-Number Alterations in Pituitary Tumors. *Endocrinology*, **2017**, 158, 2284-2291	4.8	42
95	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
94	MicroRNA Signatures and Molecular Subtypes of Glioblastoma: The Role of Extracellular Transfer. *Stem Cell Reports*, **2017**, 8, 1497-1505	8	49
93	Genomic landscape of high-grade meningiomas. *Npj Genomic Medicine*, **2017**, 2,	6.2	78

92	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. *Neuro-Oncology*, **2017**, 19, 908-917	1	14
91	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
90	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
89	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. *Neoplasia*, **2017**, 19, 75-83	6.4	23
88	Patient-derived xenografts undergo mouse-specific tumor evolution. *Nature Genetics*, **2017**, 49, 1567-1575	36.3	384
87	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. *PLoS ONE*, **2017**, 12, e0176045	3.7	22
86	Genomic profile of human meningioma cell lines. *PLoS ONE*, **2017**, 12, e0178322	3.7	30
85	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. *Neuro-Oncology*, **2017**, 19, 535-545	1	60
84	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
83	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
82	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.3	896
81	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
80	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. *Clinical Cancer Research*, **2017**, 23, 2367-2373	12.9	22
79	Landscape of Genomic Alterations in Pituitary Adenomas. *Clinical Cancer Research*, **2017**, 23, 1841-1851	12.9	64
78	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. *Nature Genetics*, **2017**, 49, 10-16	36.3	167
77	Copy-number and gene dependency analysis reveals partial copy loss of wild-type SF3B1 as a novel cancer vulnerability. *ELife*, **2017**, 6,	8.9	49
76	Copy number alterations unmasked as enhancer hijackers. *Nature Genetics*, **2016**, 49, 5-6	36.3	25
75	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. *Scientific Reports*, **2016**, 6, 25521	4.9	11

74	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. *Nature Genetics*, **2016**, 48, 848-55	36.3	135
73	Genomic landscape of intracranial meningiomas. *Journal of Neurosurgery*, **2016**, 125, 525-35	3.2	62
72	Genomic and Epigenomic Landscape in Meningioma. *Neurosurgery Clinics of North America*, **2016**, 27, 167-79	4	24
71	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, **2016**, 164, 550-63	56.2	1140
70	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. *Nature Genetics*, **2016**, 48, 273-82	36.3	154
69	MECP2 Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. *Cancer Discovery*, **2016**, 6, 45-58	24.4	35
68	MAPK activation and HRAS mutation identified in pituitary spindle cell oncocytoma. *Oncotarget*, **2016**, 7, 37054-37063	3.3	24
67	Genomic evolution and chemoresistance in germ-cell tumours. *Nature*, **2016**, 540, 114-118	50.4	100
66	Case Report: Next generation sequencing identifies a NAB2-STAT6 fusion in Glioblastoma. *Diagnostic Pathology*, **2016**, 11, 13	3	8
65	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
64	The genomic landscape of schwannoma. *Nature Genetics*, **2016**, 48, 1339-1348	36.3	74
63	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
62	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
61	ARID1A and TERT promoter mutations in dedifferentiated meningioma. *Cancer Genetics*, **2015**, 208, 345-50	2.9	57
60	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. *Neuro-Oncology*, **2015**, 17, 1344-55	1	39
59	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. *Cancer Discovery*, **2015**, 5, 1164-1177	24.4	581
58	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
57	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055

56	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. *Nature Structural and Molecular Biology*, **2015**, 22, 703-711	17.6	56
55	Pan-cancer genetic analysis identifies PARK2 as a master regulator of G1/S cyclins. *Nature Genetics*, **2014**, 46, 588-94	36.3	124
54	BET bromodomain inhibition of MYC-amplified medulloblastoma. *Clinical Cancer Research*, **2014**, 20, 912-25	12.9	227
53	SGK3 mediates INPP4B-dependent PI3K signaling in breast cancer. *Molecular Cell*, **2014**, 56, 595-607	17.6	105
52	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
51	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. *Genes and Development*, **2014**, 28, 1957-75	12.6	66
50	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. *Oncotarget*, **2014**, 5, 8083-92	3.3	46
49	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
48	Pan-cancer patterns of somatic copy number alteration. *Nature Genetics*, **2013**, 45, 1134-40	36.3	1198
47	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. *Nature Genetics*, **2013**, 45, 478-86	36.3	558
46	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. *Nature Genetics*, **2013**, 45, 285-9	36.3	397
45	Systematic interrogation of 3q26 identifies TLOC1 and SKIL as cancer drivers. *Cancer Discovery*, **2013**, 3, 1044-57	24.4	59
44	ATARiS: computational quantification of gene suppression phenotypes from multisample RNAi screens. *Genome Research*, **2013**, 23, 665-78	9.7	93
43	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 8188-93	11.5	156
42	Integrated genomic analysis of the 8q24 amplification in endometrial cancers identifies ATAD2 as essential to MYC-dependent cancers. *PLoS ONE*, **2013**, 8, e54873	3.7	56
41	Integrative analysis reveals an outcome-associated and targetable pattern of p53 and cell cycle deregulation in diffuse large B cell lymphoma. *Cancer Cell*, **2012**, 22, 359-72	24.3	148
40	Cancer vulnerabilities unveiled by genomic loss. *Cell*, **2012**, 150, 842-54	56.2	163
39	Recurrent hemizygous deletions in cancers may optimize proliferative potential. *Science*, **2012**, 337, 104-9	33.3	148

38	Amplification of phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. *BMC Proceedings*, **2012**, 6,	2.3	2
37	Absolute quantification of somatic DNA alterations in human cancer. *Nature Biotechnology*, **2012**, 30, 413-21	44.5	1229
36	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. *Nature*, **2012**, 487, 491-5	50.4	294
35	Chemical genomics identifies small-molecule MCL1 repressors and BCL-xL as a predictor of MCL1 dependency. *Cancer Cell*, **2012**, 21, 547-62	24.3	145
34	Gastrointestinal adenocarcinomas of the esophagus, stomach, and colon exhibit distinct patterns of genome instability and oncogenesis. *Cancer Research*, **2012**, 72, 4383-93	10.1	204
33	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. *Nature*, **2012**, 488, 49-56	50.4	596
32	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. *Genome Biology*, **2011**, 12, R41	18.3	1614
31	Genetic and functional studies implicate HIF1 as a 14q kidney cancer suppressor gene. *Cancer Discovery*, **2011**, 1, 222-35	24.4	283
30	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. *Nature*, **2011**, 471, 513-7	50.4	405
29	Phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. *Nature Genetics*, **2011**, 43, 869-74	36.3	788
28	Reply to Parsons: Many tumor types follow the monoclonal model of tumor initiation. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E16-E16	11.5	4
27	The landscape of somatic copy-number alteration across human cancers. *Nature*, **2010**, 463, 899-905	50.4	2590
26	Frequent and focal FGFR1 amplification associates with therapeutically tractable FGFR1 dependency in squamous cell lung cancer. *Science Translational Medicine*, **2010**, 2, 62ra93	17.5	646
25	ERG rearrangement is specific to prostate cancer and does not occur in any other common tumor. *Modern Pathology*, **2010**, 23, 1061-7	9.8	97
24	Distinct genomic aberrations associated with ERG rearranged prostate cancer. *Genes Chromosomes and Cancer*, **2009**, 48, 366-80	5	72
23	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. *Nucleic Acids Research*, **2008**, 36, 2446-56	20.1	54
22	Highly parallel identification of essential genes in cancer cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 20380-5	11.5	424
21	Modeling genomic diversity and tumor dependency in malignant melanoma. *Cancer Research*, **2008**, 68, 664-73	10.1	248

20	Characterizing the cancer genome in lung adenocarcinoma. *Nature*, **2007**, 450, 893-8	50.4	900
19	Molecular definition of breast tumor heterogeneity. *Cancer Cell*, **2007**, 11, 259-73	24.3	1135
18	Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20007-12	11.5	812
17	Single nucleotide polymorphism array analysis of cancer. *Current Opinion in Oncology*, **2007**, 19, 43-9	4.2	78
16	Epidermal growth factor receptor activation in glioblastoma through novel missense mutations in the extracellular domain. *PLoS Medicine*, **2006**, 3, e485	11.6	242
15	Allele-specific amplification in cancer revealed by SNP array analysis. *PLoS Computational Biology*, **2005**, 1, e65	5	92
14	Molecular determinants of the response of glioblastomas to EGFR kinase inhibitors. *New England Journal of Medicine*, **2005**, 353, 2012-24	59.2	1211
13	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. *Nature*, **2005**, 436, 117-22	50.4	1127
12	Overexpression, amplification, and androgen regulation of TPD52 in prostate cancer. *Cancer Research*, **2004**, 64, 3814-22	10.1	136
11	Molecular characterization of the tumor microenvironment in breast cancer. *Cancer Cell*, **2004**, 6, 17-32	24.3	1038
10	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
9	Patient-derived xenografts undergo murine-specific tumor evolution		3
8	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
7	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20
6	The whole-genome panorama of cancer drivers		38
5	Selective vulnerability of aneuploid human cancer cells to inhibition of the spindle assembly checkpoint		4
4	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
3	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities		1